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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:09:40 ; Search time 48 Seconds
(without alignments)
23.148 Million cell updates/sec

Title: US-09-772-819-18
Perfect score: 41
Sequence: 1 RYAHPP 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_193Jun03.*
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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
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23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	7	AAW65614	Angiotensin II ana
2	41	100.0	7	AAW64744	Angiotensin III pe
3	41	100.0	7	AAW71127	Peptide used to ac
4	41	100.0	7	AAW49600	Angiotensin analog
5	41	100.0	7	AAW42353	Angiotensin II ana
6	41	100.0	7	AAW30554	Amino acid sequenc
7	41	100.0	7	AAW30598	Amino acid sequenc
8	41	100.0	7	AAW32749	Angiotensin II ana
9	41	100.0	7	AAW32729	Angiotensin II ana

10	41	100.0	7	20	AAW33783	Angiotensin II (AI
11	41	100.0	7	20	AAW15359	Angiotensin II (AI
12	41	100.0	7	20	AAW15319	Angiotensin II (AI
13	41	100.0	7	21	AAW27418	Angiotensin II ana
14	41	100.0	7	21	AAW28116	Angiotensin II ana
15	41	100.0	7	21	AAW84140	Amino acid sequenc
16	41	100.0	7	21	AAW77053	Angiotensin II (AI
17	41	100.0	7	21	AAW57415	Angiotensin peptid
18	41	100.0	7	22	AAE08886	AI peptide analog
19	41	100.0	7	22	AAE03003	Human angiotensin
20	41	100.0	7	22	AAE03166	Human angiotensin
21	41	100.0	7	23	AAE19202	Angiotensin II pep
22	41	100.0	7	23	AAW5782	Angiotensin AI pe
23	41	100.0	7	24	ABU11429	Angiotensin II ana
24	41	100.0	7	24	ABU12346	Angiotensin II (AI
25	37	90.2	7	19	AAW65609	Angiotensin II ana
26	37	90.2	7	19	AAW64743	Angiotensin III pe
27	37	90.2	7	19	AAW64740	Angiotensin II pep
28	37	90.2	7	19	AAW65634	Angiotensin III an
29	37	90.2	7	19	AAW65613	Angiotensin II ana
30	37	90.2	7	19	AAW71126	Peptide used to ac
31	37	90.2	7	19	AAW71122	Peptide used to ac
32	37	90.2	7	20	AAW49597	Angiotensin analog
33	37	90.2	7	20	AAW49599	Angiotensin analog
34	37	90.2	7	20	AAW33912	Angiotensin II ana
35	37	90.2	7	20	AAW42352	Angiotensin II ana
36	37	90.2	7	20	AAW30551	Amino acid sequenc
37	37	90.2	7	20	AAW30553	Amino acid sequenc
38	37	90.2	7	20	AAW30576	Amino acid sequenc
39	37	90.2	7	20	AAW30595	Amino acid sequenc
40	37	90.2	7	20	AAW30597	Angiotensin II ana
41	37	90.2	7	20	AAW32726	Angiotensin II ana
42	37	90.2	7	20	AAW32728	Angiotensin II ana
43	37	90.2	7	20	AAW33780	Angiotensin II (AI
44	37	90.2	7	20	AAW33782	Angiotensin II (AI
45	37	90.2	7	20	AAW15356	Angiotensin II (AI

ALIGNMENTS

RESULT 1
AAW65614
ID AAW65614 standard; peptide; 7 AA.
AC AAW65614;
XX
DT 09-NOV-1998 (first entry)
XX
DE Angiotensin II analogue.
XX
KW angiotensin II; skin graft; AI analogue; tissue repair; vasoconstrictor;
XX wound healing.
XX Synthetic.
OS Homo sapiens.
XX
PM WO9826795-A1.
XX
XX 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23461.
XX
PR 15-DEC-1997; 97US-0990664.
XX 16-DEC-1996; 96US-0028310.
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Dizerega GS, Rodgers KE;
XX WPI; 1998-362518/31.
XX
PT Promoting incorporation of skin graft onto underlying tissue -

PT comprises pre-treating graft with angiotensin II, or analogue or
PT peptide fragment

XX Disclosure; Page 7; 82pp; English.

XX The invention relates to the use of angiotensin II (AII), AII analogues,
CC AII fragments and AII fragment analogues for promoting incorporation of a
CC skin graft into underlying tissue of a mammal. The peptides are effective
CC in accelerating the growth or healing of skin grafts and in accelerating
CC re-epithelialisation and tissue repair, even at very low concentrations.
CC They can significantly accelerate the rate of healing at nanomolar levels
CC in vivo. AII accelerates wound repair by increased neovascularisation,
CC growth factor release, re-epithelialisation, extracellular matrix production
CC and increased flow of blood and nutrients to the injured tissue. Use of
CC the above peptides other than AII itself (an extremely potent vaso-
CC constrictor) may avoid the side-effects of AII, such as increase in blood
CC pressure and thirst. The present sequence represents an angiotensin
CC II analogue.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7

DB 1 RYVAHPF 7

RESULT 2

AAW64744

ID AAW64744 standard; peptide; 7 AA.

AC AAW64744;

DT 02-NOV-1998 (first entry)

DE Angiotensin III peptide #2.

XX Proliferation; mesenchymal stem cell; lineage-specific cell;
KW haematopoietic; cell culture; transplantation; treatment; malignant;
KW inherited disease; angiotensinogen; angiotensin I; angiotensin III.

XX Synthetic.

OS Homo sapiens.

XX WO9832457-A2.

XX 30-JUL-1998.

XX 26-JAN-1998; 98WO-US01552.

XX 23-JAN-1998; 98US-0066593.

XX 28-JAN-1997; 97US-0036507.

XX 08-MAY-1997; 97US-0046859.

XX 28-OCT-1997; 97US-0063684.

XX 31-OCT-1997; 97US-0063910.

XX 18-NOV-1997; 97US-0065612.

XX 26-NOV-1997; 97US-0066593.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX diZerega G, Rodgers KE;

XX WPI; 1998-437044/37.

XX Promoting haematopoietic and mesenchymal cell proliferation and
PT differentiation - by contacting the cells with angiotensinogen,
PT angiotensin I or II, or analogues or fragments of these

XX Claim 37; Page 15; 114pp; English.

CC AAW64728-W64763 are peptides used in a novel method for accelerating the
CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
CC lineage-specific cells or mesenchymal lineage-specific cells. The method
CC involves contacting the cells with an active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R1-R8 in
CC the sequence of formula R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
CC Ala, Leu, norLeu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane
CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(PCO)2, Thr, Ser, homoser or
CC azATyr, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or
CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr. Ra and Rb are
CC not defined in the specification, the peptide bond between Ra and Rb is
CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
CC terminal Tyr group. A second active agent comprising a sequence
CC consisting of at least three contiguous amino acids of groups R2-R8 in
CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also
CC described. The inventions are particularly useful in cell culture
CC mediums. These cells may be used in transplantation techniques for
CC treatment of malignant or inherited diseases. The formulae represent
CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),
CC or AII AT2 type 2 receptor agonists.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7

DB 1 RYVAHPF 7

RESULT 3

AAW71127

ID AAW71127 standard; peptide; 7 AA.

XX AAW71127;

XX 27-OCT-1998 (first entry)

XX Peptide used to accelerate thermal wound healing.

XX Angiotensin; AII; acceleration; thermal wound healing; human;
KW growth factor release; neovascularisation; re-epithelialisation;
KW extracellular matrix production.

XX Synthetic.

XX WO9833813-A2.

XX 06-AUG-1998.

XX 04-FEB-1998; 98WO-US02049.

XX 04-FEB-1997; 97US-0037166.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX DiZerega G, Rodgers KE;

XX WPI; 1998-437391/37.

XX Methods for accelerating thermal wound healing in humans - using
PT angiotensinogen II and AII analogues

XX Claim 9; Page 10; 58pp; English.

XX AAW71110-27 represent peptide used in the method of the invention. The
CC specification describes a method of accelerating thermal wound healing
CC in humans. The method comprises applying to the thermally injured tissue
CC an amount of at least one active agent which comprises the peptides

CC AAW71115-27. The method can be used to promote the healing of thermal
 CC wounds by accelerating growth factor release, neovascularisation,
 CC re-epithelialisation and extracellular matrix production. The sequences
 CC are analogues of the angiotensin or angiotensinogen family of proteins.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 |||||
 Db 1 RYVAHPF 7

RESULT 4
 AAY49600
 ID AAY49600 standard; peptide; 7 AA.

XX
 AC AAY49600;

XX 13-JAN-2000 (first entry)

XX Angiotensin analogue peptide SEQ ID NO:18.

XX Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
 KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
 XX
 OS Synthetic.

XX WO9952540-A1.

XX 21-OCT-1999.

XX 07-APR-1999; 99WO-US07654.

XX 09-APR-1998; 98US-0081262.

XX 12-JUN-1998; 98US-0089024.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-620285/53.

XX Treating or preventing infections in mammals using peptides derived
 from angiotensin or angiotensin receptor agonists .

XX Claim 2; Page 12; 91pp; English.

XX The present invention describes a method for treating or preventing
 infections in mammals by administering peptides (A) that are fragments
 or analogues (or their fragments) of angiotensinogen, angiotensins I or
 II, or angiotensin II AT 2-type receptor agonists. (A) contain at least
 3 consecutive amino acids (aa) from the sequence (S1):

CC R1-R2-R3-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
 CC X = Hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane
 CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH 2), Gly,
 CC Asp(NH 2) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
 CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
 CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr;
 CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
 CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
 CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =
 CC sequences having R4 as a terminal Tyr residue are excluded. The method
 CC is particularly used in cases of bacterial infection (e.g. septic shock,
 CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
 CC parasitic infections. AAY49586 to AAY49623 represent specifically
 CC claimed examples of (A).
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 |||||
 Db 1 RYVAHPF 7

RESULT 5
 AAY42353
 ID AAY42353 standard; peptide; 7 AA.

XX
 AC AAY42353;

XX 29-NOV-1999 (first entry)

XX Angiotensin II analogue 22.

XX embryonic stem cell; ES; angiotensin; totipotent cell;
 KW gene therapy; replacement therapy; angiotensin II; AII;
 KW analogue.

XX Homo sapiens.

XX WO9942122-A1.

XX 26-AUG-1999.

XX 16-FEB-1999; 99WO-US03243.

XX 19-FEB-1998; 98US-0075179.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1999-527419/44.

XX Promoting embryonal cell proliferation, using angiotensinogen and
 angiotensin peptides, analogs or fragments

XX Claim 2; Page 10; 76pp; English.

XX This is the amino acid sequence of the Angiotensin II analogue, 22.
 CC The formation of Angiotensin II (AII) is initiated by the action of
 CC renin on the plasma substrate angiotensinogen.

CC This results in Angiotensin I (AI) which then converted to AII by the
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu
 CC residues from AI (AAY42372).

CC The active agents Angiotensinogen, Angiotensin I (AI), AI
 CC analogs, AI fragments and analogs, Angiotensin II (AII), AII analogs,
 CC AII fragments or analogs, or AII AT2 type 2 receptor agonists can
 CC rapidly provide a large population of ESCs (Embryonic Stem Cell) for use
 CC in replacement therapy. Similarly, methods that increase in vivo

CC proliferation of ESCs will enhance the utility of replacement therapy by
 CC rapidly increasing local concentration of the stem cells and their
 CC progeny at the site of therapy. The method also increases the potential
 CC utility of ESCs as vehicles for gene therapy in certain disorders by
 CC more efficiently providing a large number of such cells for transfection,
 CC and also by providing a more efficient means to rapidly expand
 CC transfected ESCs.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 |||||
 Db 1 RYVAHPF 7

RESULT 6
 AAY30554
 ID AAY30554 standard; peptide; 7 AA.
 XX AC AAY30554;
 XX DT 18-NOV-1999 (first entry)
 XX DE Amino acid sequence of an angiotensin II analogue.
 XX KW Angiotensin; analogue; tissue equivalent; cell proliferation.
 XX OS Synthetic.
 XX PN W09946285-A2.
 XX PD 16-SEP-1999.
 XX PF 11-MAR-1999; 99WO-US05261.
 XX PR 11-MAR-1998; 98US-0077499.
 XX PR 12-JUN-1998; 98US-0083064.
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX PI Rodgers KE, Dizerega G;
 XX WPI; 1999-551360/46.
 XX PT An improved method for producing a tissue equivalent with angiotensin I
 PT and II derived active agents -
 XX PS Claim 2; Page 62; 83pp; English.
 XX CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AI
 CC fragments and AI analogues. The peptides are used in the method
 CC of the invention. The specification describes an improved method
 CC for producing a tissue equivalent. The method comprises contacting
 CC the tissue equivalent with angiotensin I and II derived active
 CC agents. The methods are used for production and culture of tissue
 CC equivalents (three-dimensional cell and tissue culture systems),
 CC chosen from skin, cartilage, ligament, collagen lattice, liver and
 CC vascular graft, dermis, bone, bone marrow, pancreas, heart valve,
 CC kidney tissue equivalents. The methods and tissue culture systems
 CC are used for the long-term proliferation of cells and tissues
 CC in an in vitro environment that more closely approximates that found
 CC in vivo.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 Db 1 RYVAHPF 7

RESULT 7
 AAY30598
 ID AAY30598 standard; peptide; 7 AA.
 XX AC AAY30598;
 XX DT 18-NOV-1999 (first entry)
 XX DE Amino acid sequence of an angiotensin II (AII) analogue.
 XX KW Angiotensin; analogue; radiation mitigation; tissue damage;
 KW radiation therapy; bone marrow transplantation;
 KW megakaryocyte production; platelet production; cancer therapy;

KW gene therapy; hematopoietic disorder.
 XX OS Synthetic.
 XX PN W09945945-A1.
 XX PD 16-SEP-1999.
 XX PF 08-MAR-1999; 99WO-US05194.
 XX PR 10-MAR-1998; 98US-0077382.
 XX PR 09-APR-1998; 98US-0081262.
 XX PR 30-APR-1998; 98US-0083670.
 XX PR 19-JUN-1998; 98US-0090096.
 XX PR 22-JUN-1998; 98US-0090216.
 XX PR 11-SEP-1998; 98US-0099957.
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX PA (RODG/) RODGERS K E.
 XX PA (DIZE/) DIZEREKA G.
 XX PI Rodgers KE, Dizerega G;
 XX WPI; 1999-551209/46.
 XX PT Use of angiotensin and angiotensin type peptides, for mitigating
 PT radiation induced tissue damage, improving bone marrow transplantation
 PT and promoting megakaryocyte and platelet production -
 XX PS Claim 2; Page 97; 116pp; English.
 XX CC AAY30583-330620 represent angiotensin I (AI) and angiotensin (II), AII
 CC fragments and AII analogues. The peptides are used in the method
 CC of the invention. The specification describes a method for mitigating
 CC radiation induced tissue damage, improving the effectiveness of
 CC radiation therapy, to support bone marrow transplantation, and
 CC promoting megakaryocyte production and mobilization and platelet
 CC production. The method comprises administration of the present peptides.
 CC The methods can be used to mitigate radiation induced tissue damage, to
 CC improve the effectiveness of radiation therapy, to support bone marrow
 CC transplantation, and to promote megakaryocyte production and
 CC mobilization and platelet production. They are used particularly in
 CC cancer therapy. They can also be used to provide megakaryocytes as
 CC vehicles for gene therapy in hematopoietic disorders, by providing a
 CC more efficient means to rapidly expand transduced megakaryocytes.
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 Db 1 RYVAHPF 7

RESULT 8
 AAY32749
 ID AAY32749 standard; peptide; 7 AA.
 XX AC AAY32749;
 XX DT 09-NOV-1999 (first entry)
 XX DE Angiotensin II analogue 22.
 XX KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;
 KW hepatocarcinoma; hepatectomy; transplantation.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX WO9939743-A2.
 XX 12-AUG-1999.
 XX 08-FEB-1999; 99WO-US02618.
 XX 13-NOV-1998; 98US-0108412.
 XX 09-FEB-1998; 98US-0074104.
 XX (DIZE/) DIZEREGA G.
 XX (RODG/) RODGERS K E.
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX Dizerega G, Rodgers KE;
 XX WPI; 1999-508461/42.
 XX Hepatic cell proliferation with angiotensin I and II derived active agents, useful for regeneration of liver after resection
 XX Claim 2; Page 11; 66pp; English.
 XX Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The peptides are derived from the AII peptide (AAY32750). AII increases mitogenesis and chemotaxis in cultured cells, and also increases the release of growth factors and extracellular matrices. AII has also been shown to increase the proliferation of certain cell types. The AII analogue peptides can be used as the active agent in a method for promoting hepatic cell proliferation and differentiation. The method involves contacting the hepatic cells with an amount effective enough to promote proliferation of any of the peptides. This method is useful in liver regeneration following resection of hepatocarcinomas, hepatitis infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic failure, hepatocyte transplantation, liver transplantation and other hepatic disorders where rapid regeneration of the liver is desirable. The methods are also useful in rapidly providing a large population of hepatic cells for use in cell therapy and for providing a large population of transfectected hepatic cells for use in gene therapy.

XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYVAHPF 7
 Db 1 RYVAHPF 7
 RESULT 9
 AAY32729
 ID AAY32729 standard; peptide; 7 AA.
 AC AAY32729;
 DT 09-NOV-1999 (first entry)
 DE Angiotensin II analogue 21.
 KW Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;
 KW hepatocarcinoma; hepatectomy; transplantation.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9939743-A2.
 XX 12-AUG-1999.
 XX 08-FEB-1999; 99WO-US02618.

XX 13-NOV-1998; 98US-0108412.
 XX 09-FEB-1998; 98US-0074104.
 XX (DIZE/) DIZEREGA G.
 XX (RODG/) RODGERS K E.
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX Dizerega G, Rodgers KE;
 XX WPI; 1999-508461/42.
 XX Hepatic cell proliferation with angiotensin I and II derived active agents, useful for regeneration of liver after resection
 XX Claim 2; Page 11; 66pp; English.
 XX Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The peptides are derived from the AII peptide (AAY32750). AII increases mitogenesis and chemotaxis in cultured cells, and also increases the release of growth factors and extracellular matrices. AII has also been shown to increase the proliferation of certain cell types. The AII analogue peptides can be used as the active agent in a method for promoting hepatic cell proliferation and differentiation. The method involves contacting the hepatic cells with an amount effective enough to promote proliferation of any of the peptides. This method is useful in liver regeneration following resection of hepatocarcinomas, hepatitis infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic failure, hepatocyte transplantation, liver transplantation and other hepatic disorders where rapid regeneration of the liver is desirable. The methods are also useful in rapidly providing a large population of hepatic cells for use in cell therapy and for providing a large population of transfectected hepatic cells for use in gene therapy.

XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYVAHPF 7
 Db 1 RYVAHPF 7
 RESULT 10
 AAY33783
 ID AAY33783 standard; peptide; 7 AA.
 AC AAY33783;
 DT 09-NOV-1999 (first entry)
 DE Angiotensin II (AII) octapeptide analogue 21.
 KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;
 KW Parkinson's disease; neuron replacement therapy.
 XX Homo sapiens.
 OS WO9942123-A1.
 XX 26-AUG-1999.
 XX 19-FEB-1999; 99WO-US03772.
 XX 19-FEB-1998; 98US-0075232.
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX Dizerega G, Rodgers KE;

DR WPI; 1999-527420/44.

XX Promoting neuronal cell proliferation and differentiation

XX PS Claim 2; Page 12; 62pp; English.

CC Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin II (AII) octapeptide (AAY33769) and they have AT2 agonist activity. The application of angiotensin to wound tissue significantly increases the rate of wound healing. AII is known to increase mitogenesis and chemotaxis in cultured cells, and also increases their release of growth factors and extracellular matrices, implicating it in cell growth and differentiation. AT2 receptors are receptors for AII and are thought to be involved in the mediation of the cell differentiation effects of AII. Peptides AAY33769-Y33802 are used in a method for promoting neuronal cell proliferation or differentiation. This method is useful in the treatment of Alzheimer's and Parkinson's diseases by neuron replacement therapy.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7

DB 1 RYVAHPF 7

RESULT 11

AAV15359
ID AAY15359 standard; peptide; 7 AA.

XX AC AAY15359;

XX DT 09-NOV-1999 (first entry)

XX DE Angiotensin II (AII) analogue 22.

XX KW burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;
XX KW AII; analogue; chronic renal failure; cancer; bone marrow.

XX OS Synthetic.

XX OS Homo sapiens.

XX FN WO9940106-A2.

XX FD 12-AUG-1999.

XX PF 08-FEB-1999; 99WO-US02648.

XX PR 09-DEC-1998; 98US-0111535.

XX PR 09-FEB-1998; 98US-C0074106.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX WPI; 1999-508486/42.

XX Promoting erythropoiesis with angiotensin I and II derived active
XX PT agents, useful for treatment of, e.g. congenital or acquired
XX PT aplastic or hypoplastic anemia

XX PS Claim 2; Page 11; 76pp; English.

XX This sequence is an angiotensin II (AII) analogue. Similar sequences
XX also based on the AII peptide have been tested against each other. AII
XX and a negative control. These active agents have been shown to affect
XX the levels of BFU-E (burst forming units-erythroid) in culture.
XX The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)
XX augment erythropoiesis by potentiating erythropoietin-induced

CC differentiation. Increasing the rate of erythropoiesis improves clinical
CC benefits for the treatment of congenital or acquired aplastic or
CC hypoplastic anemia associated with chronic renal failure, end-stage renal
CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,
CC bone marrow transplantation and chronic diseases.

CC The active agents permit the use of smaller doses of erythropoietin
CC therefore decreasing treatment costs.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7

DB 1 RYVAHPF 7

RESULT 12

AAV15319

ID AAY15319 standard; peptide; 7 AA.

XX AC AAY15319;

XX DT 09-NOV-1999 (first entry)

XX DE Angiotensin II (AII) analogue 22.

XX KW angiotensin; angiotensin II; AII; wound healing; scarring;
XX KW tissue repair; agonist; analogue.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9940107-A2.

XX PD 12-AUG-1999.

XX PF 08-FEB-1999; 99WO-US02725.

XX PR 09-FEB-1998; 98US-0074105.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Dizerega G, Rodgers KE;

XX WPI; 1999-508487/42.

XX Epithelial stem cell and keratinocyte proliferation with angiotensin
XX I and II derived active agents, useful for treatment of skin wounds

XX PS Claim 2; Page 12; 70pp; English.

XX This is the amino acid sequence of an Angiotensin II analogue. This and
XX other similar analogues (AAY15306 to AAY15316 and AAY15317 to AAY15341)
XX can be used to promote the proliferation of epithelial stem cells and
XX keratinocytes leading to a more rapid and efficient cellular response to
XX stratified epithelial injury. The angiotensin analogues are derived from
XX an octapeptide present in humans and other species which has the
XX sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as
XX angiotensin II (AII). This is formed by the action of renin on the
XX plasma substrate angiotensinogen, the product of this reaction is a
XX decapeptide called angiotensin I (AI) which is converted to AII by the
XX converting enzyme angiotensinase which removes the C-terminal His-Leu
XX residues from AI (AAY15339).

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PF 12-AUG-1999; 99MO-US18374.
 XX
 PR 13-AUG-1998; 98US-0096414.
 PR 18-SEP-1998; 98US-0101024.
 XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 XX Rodgers K, Dizerega G;
 PI
 XX WPI; 2000-237409/20.
 DR
 XX
 XX Increasing blood flow to ischemic tissue for minimizing cardiac
 PT remodelling and development of congestive heart failure involves
 PT administration of an active agent -
 PT
 XX
 XX Claim 2; Page 45; 56pp; English.
 PS
 XX
 XX The present sequence represents an angiotensin II analogue. The
 CC specification also describes peptides derived from angiotensinogen,
 CC angiotensin I, angiotensin II, angiotensin III, and their analogues.
 CC The peptides are used for increasing blood flow to ischemic tissue.
 CC The peptides are angiotensin stimulators. The peptides are useful for
 CC increasing blood flow to ischemic tissue by stimulating angiogenesis,
 CC and minimizing cardiac remodelling and development of congestive heart
 CC disease following a ischemic myocardial infarction. The stimulation of
 CC angiogenesis is also useful for embryonic development, wound healing
 CC and treating chronic inflammatory disease.
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYVAHPF 7
 Db 1 RYVAHPF 7
 |||||
 |||||
 Search completed: November 5, 2003, 18:13:49
 Job time : 49 secs

GetCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:12:56 ; Search time 20 Seconds
(without alignments)
14.809 Million cell updates/sec

Title: US-09-772-819-18

Perfect score: 41
Sequence: 1 RYAHFP 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 3287.7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	41	100.0	7	3	US-08-990-664-19
2	41	100.0	7	3	US-09-373-962-18
3	41	100.0	7	3	US-09-245-680-18
4	41	100.0	7	3	US-09-198-806C-18
5	41	100.0	7	3	US-09-352-191-18
6	41	100.0	7	4	US-09-012-400-18
7	41	100.0	7	4	US-09-264-563-18
8	41	100.0	7	4	US-09-307-940B-19
9	41	100.0	7	4	US-09-657-890-18
10	41	100.0	7	4	US-09-266-293A-18
11	41	100.0	7	4	US-09-716-394-18
12	37	90.2	7	3	US-08-990-664-14
13	37	90.2	7	3	US-08-990-664-18
14	37	90.2	7	3	US-08-990-664-39
15	37	90.2	7	3	US-09-210-249-10
16	37	90.2	7	3	US-09-373-962-13
17	37	90.2	7	3	US-09-373-962-17
18	37	90.2	7	3	US-09-245-680-13
19	37	90.2	7	3	US-09-245-680-17
20	37	90.2	7	3	US-09-198-806C-13
21	37	90.2	7	3	US-09-198-806C-17
22	37	90.2	7	3	US-09-352-191-13
23	37	90.2	7	3	US-09-352-191-17
24	37	90.2	7	4	US-09-012-400-13
25	37	90.2	7	4	US-09-012-400-17
26	37	90.2	7	4	US-09-264-563-13
27	37	90.2	7	4	US-09-264-563-17

28	37	90.2	7	4	US-09-698-354-10	Sequence 10, Appl
29	37	90.2	7	4	US-09-307-940B-13	Sequence 13, Appl
30	37	90.2	7	4	US-09-307-940B-17	Sequence 13, Appl
31	37	90.2	7	4	US-09-657-890-13	Sequence 13, Appl
32	37	90.2	7	4	US-09-657-890-17	Sequence 17, Appl
33	37	90.2	7	4	US-09-266-293A-13	Sequence 13, Appl
34	37	90.2	7	4	US-09-266-293A-17	Sequence 17, Appl
35	37	90.2	7	4	US-09-266-293A-40	Sequence 40, Appl
36	37	90.2	7	4	US-09-716-394-13	Sequence 13, Appl
37	37	90.2	7	4	US-09-716-394-17	Sequence 17, Appl
38	37	90.2	8	1	US-08-594-117-3	Sequence 3, Appl
39	37	90.2	8	1	US-08-594-117-4	Sequence 4, Appl
40	37	90.2	8	2	US-08-623-833B-2	Sequence 2, Appl
41	37	90.2	8	3	US-08-990-664-20	Sequence 20, Appl
42	37	90.2	8	3	US-08-990-664-21	Sequence 21, Appl
43	37	90.2	8	3	US-08-990-664-35	Sequence 35, Appl
44	37	90.2	8	3	US-09-210-249-6	Sequence 6, Appl
45	37	90.2	8	3	US-09-373-962-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-990-664-19
; Sequence 19, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; TITLE OF INVENTION: IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92860

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,664
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,310
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: USC012.001A
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-990-664-19

Query Match 100.0%; Score 41; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYAHPPF 7
 Db 1 RYAHPPF 7

RESULT 2

US-09-373-962-18
 ; Sequence 18, Application US/09373962
 ; Patent No. 6177407
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gere
 ; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
 ; FILE REFERENCE: 98364A
 ; CURRENT APPLICATION NUMBER: US/09/373.962
 ; CURRENT FILING DATE: 1999-08-13
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:All analogue
 US-09-373-962-18

Query Match 100.0%; Score 41; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYAHPPF 7
 Db 1 RYAHPPF 7

RESULT 3

US-09-245-680-18
 ; Sequence 18, Application US/09245680B
 ; Patent No. 6239109
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gere
 ; TITLE OF INVENTION: Method of Promoting Erythropoiesis
 ; FILE REFERENCE: 980098
 ; CURRENT APPLICATION NUMBER: US/09/245.680B
 ; CURRENT FILING DATE: 1999-02-08
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:All analogue
 US-09-245-680-18

Query Match 100.0%; Score 41; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYAHPPF 7
 Db 1 RYAHPPF 7

RESULT 4

US-09-198-806C-18
 ; Sequence 18, Application US/09198806C
 ; Patent No. 6248587
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gere
 ; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem

; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation
 ; FILE REFERENCE: 97,017-F1
 ; CURRENT APPLICATION NUMBER: US/09/198.806C
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:All analogue
 US-09-198-806C-18

Query Match 100.0%; Score 41; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYAHPPF 7
 Db 1 RYAHPPF 7

RESULT 5

US-09-352-191-18
 ; Sequence 18, Application US/09352191
 ; Patent No. 6258778
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gere
 ; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
 ; TITLE OF INVENTION: Growth and Repair
 ; FILE REFERENCE: 98365B
 ; CURRENT APPLICATION NUMBER: US/09/352.191
 ; CURRENT FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:All analogue
 US-09-352-191-18

Query Match 100.0%; Score 41; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYAHPPF 7
 Db 1 RYAHPPF 7

RESULT 6

US-09-012-400-18
 ; Sequence 18, Application US/09012400D
 ; Patent No. 635195
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gere
 ; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
 ; TITLE OF INVENTION: Proliferation and Differentiation
 ; FILE REFERENCE: 97,017-G
 ; CURRENT APPLICATION NUMBER: US/09/012.400D
 ; CURRENT FILING DATE: 1998-01-23
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-012-400-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPP 7
Db 1 RVYAHPP 7

RESULT 7
US-09-264-563-18
; Sequence 18, Application US/09264563A
; Patent No. 6455500
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: gizerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017KJ
; CURRENT APPLICATION NUMBER: US/09/264,563A
; CURRENT FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue

US-09-264-563-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPP 7
Db 1 RVYAHPP 7

RESULT 8
US-09-307-940B-18
; Sequence 18, Application US/09307940B
; Patent No. 6475988
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: gizerega, Gere
; TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After
; FILE REFERENCE: 97017P1
; CURRENT APPLICATION NUMBER: US/09/307,940B
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPP 7
Db 1 RVYAHPP 7

RESULT 9
US-09-657-890-18
; Sequence 18, Application US/09657890
; Patent No. 6482800
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: gizerega, Gere
; TITLE OF INVENTION: Methods to Stimulate Angiogenesis
; FILE REFERENCE: 98364A1
; CURRENT APPLICATION NUMBER: US/09/657,890
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPP 7
Db 1 RVYAHPP 7

RESULT 10
US-09-266-293A-18
; Sequence 18, Application US/09266293A
; Patent No. 6498138
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: gizerega, Gere
; TITLE OF INVENTION: Method of Promoting Production of Living Tissue
; FILE REFERENCE: 98094b
; CURRENT APPLICATION NUMBER: US/09/266,293A
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPP 7
Db 1 RVYAHPP 7

RESULT 11
US-09-716-394-18
; Sequence 18, Application US/09716394
; Patent No. 6566335
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rodgers, Kathleen
; APPLICANT: gizerega, Gere
; TITLE OF INVENTION: Methods for Mobilizing Hematopoietic Progenitor Cells from Bone
; FILE REFERENCE: 97,017-P8
; CURRENT APPLICATION NUMBER: US/09/716,394

; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/084,908
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: US 60/092,633
; PRIOR FILING DATE: 1998-07-13
; PRIOR APPLICATION NUMBER: US 09/307,940
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Ala4 A111
US-09-716-394-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 12
US-08-990-664-14
; Sequence 14, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 4...4

; OTHER INFORMATION: Position 4 is notLeu
US-08-990-664-14

Query Match 90.2%; Score 37; DB 3; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 13
US-08-990-664-18
; Sequence 18, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:

; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-990-664-18

Query Match 90.2%; Score 37; DB 3; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 14
US-08-990-664-39
; Sequence 39, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen

APPLICANT: diZerega, Gere
TITLE OF INVENTION: METHOD OF PROMOTING HEALING
IN SKIN GRAFTS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,664
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,310
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/SOCKET NUMBER: USC02.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-990-664-39

Query Match 90.2%; Score 37; DB 3; Length 7;
Best Local Similarity 85.7%; Pred.No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
| | | | |
Db 1 RYVXHPF 7

RESULT 15
US-09-210-249-10
; Sequence 10, Application US/09210249A
; Patent No. 6165978
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: WOUND HEALING COMPOSITIONS
; FILE REFERENCE: USC013, 001A
; CURRENT APPLICATION NUMBER: US/09/210,249A
; CURRENT FILING DATE: 1998-12-11
; EARLIER APPLICATION NUMBER: 60/069,662
; EARLIER FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)

; OTHER INFORMATION: Xaa(4) is norLeu
US-09-210-249-10

Query Match 90.2%; Score 37; DB 3; Length 7;
Best Local Similarity 85.7%; Pred.No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
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Db 1 RYVXHPF 7

Search completed: November 5, 2003, 18:19:44
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:15:01 ; Search time 40 Seconds
(without alignments)
30.056 Million cell updates/sec

Title: US-09-772-819-18

Perfect score: 41

Sequence: 1 RVYAHPP 7

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000003

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	41	100.0	7	10 US-09-837-697A-18	Sequence 18, Appl
3	41	100.0	7	10 US-09-900-936-18	Sequence 18, Appl
4	41	100.0	7	12 US-09-772-819-18	Sequence 18, Appl
5	41	100.0	7	16 US-10-341-001-18	Sequence 18, Appl
6	37	90.2	7	9 US-09-771-192-13	Sequence 13, Appl
7	37	90.2	7	9 US-09-771-192-17	Sequence 17, Appl
8	37	90.2	7	10 US-09-837-697A-13	Sequence 13, Appl
9	37	90.2	7	10 US-09-837-697A-17	Sequence 17, Appl
10	37	90.2	7	10 US-09-900-936-13	Sequence 13, Appl
11	37	90.2	7	12 US-09-900-936-17	Sequence 17, Appl
12	37	90.2	7	12 US-09-772-819-13	Sequence 13, Appl
13	37	90.2	7	12 US-09-772-819-17	Sequence 17, Appl
14	37	90.2	7	16 US-10-341-001-13	Sequence 13, Appl
15	37	90.2	7	16 US-10-341-001-17	Sequence 17, Appl

16	37	90.2	8	9 US-09-771-192-19	Sequence 19, Appl
17	37	90.2	8	9 US-09-771-192-20	Sequence 20, Appl
18	37	90.2	8	9 US-09-771-192-34	Sequence 34, Appl
19	37	90.2	8	10 US-09-837-697A-19	Sequence 19, Appl
20	37	90.2	8	10 US-09-837-697A-20	Sequence 20, Appl
21	37	90.2	8	10 US-09-837-697A-34	Sequence 34, Appl
22	37	90.2	8	10 US-09-900-936-19	Sequence 19, Appl
23	37	90.2	8	10 US-09-900-936-20	Sequence 20, Appl
24	37	90.2	8	10 US-09-900-936-34	Sequence 34, Appl
25	37	90.2	8	12 US-09-772-819-19	Sequence 19, Appl
26	37	90.2	8	12 US-09-772-819-20	Sequence 20, Appl
27	37	90.2	8	12 US-09-772-819-34	Sequence 34, Appl
28	37	90.2	8	16 US-10-341-001-19	Sequence 19, Appl
29	37	90.2	8	16 US-10-341-001-20	Sequence 20, Appl
30	37	90.2	8	16 US-10-341-001-34	Sequence 34, Appl
31	36	87.8	7	9 US-09-771-192-2	Sequence 2, Appl
32	36	87.8	7	10 US-09-837-697A-2	Sequence 2, Appl
33	36	87.8	7	10 US-09-900-936-2	Sequence 2, Appl
34	36	87.8	7	12 US-09-772-819-2	Sequence 2, Appl
35	36	87.8	7	15 US-10-197-984-11	Sequence 11, Appl
36	36	87.8	7	16 US-10-341-001-2	Sequence 2, Appl
37	36	87.8	8	9 US-09-785-177-1	Sequence 1, Appl
38	36	87.8	8	9 US-09-771-192-1	Sequence 1, Appl
39	36	87.8	8	9 US-09-771-192-22	Sequence 22, Appl
40	36	87.8	8	9 US-09-771-192-26	Sequence 26, Appl
41	36	87.8	8	9 US-09-771-192-30	Sequence 30, Appl
42	36	87.8	8	9 US-09-771-192-32	Sequence 32, Appl
43	36	87.8	8	9 US-09-771-192-45	Sequence 45, Appl
44	36	87.8	8	10 US-09-950-692-7	Sequence 7, Appl
45	36	87.8	8	10 US-09-784-005-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-771-192-18
; Sequence 18, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-771-192-18

Query Match 100.0%; Score 41; DB 9; Length 7;
Best Local Similarity 100.0%; Pred No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPP 7
| | | | |
Db 1 RVYAHPP 7

RESULT 2

US-09-837-697A-18
; Sequence 18, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: dizerega, Gere

; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; TITLE OF INVENTION: Differentiation
; FILE REFERENCE: 97,017-F1A
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: All analogue
US-09-837-697A-18

Query Match 100.0%; Score 41; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 3

US-09-900-936-18
; Sequence 18, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-900-936-18

Query Match 100.0%; Score 41; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 4

US-09-772-819-18
; Sequence 18, Application US/09772819
; Publication No. US20030199434A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; TITLE OF INVENTION: Growth and Repair
; FILE REFERENCE: 98365b
; CURRENT APPLICATION NUMBER: US/09/772,819
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-772-819-18

Query Match 100.0%; Score 41; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 5

US-10-341-001-18
; Sequence 18, Application US/10341001
; Publication No. US20030130196A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K5
; CURRENT APPLICATION NUMBER: US/10/341,001
; CURRENT FILING DATE: 2003-01-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-10-341-001-18

Query Match 100.0%; Score 41; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

RESULT 6

US-39-771-192-13
; Sequence 13, Application US/097711192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-39-771-192-13

Query Match 90.2%; Score 37; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 1 RYVAHPF 7

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Db 1 RYXHPF 7

RESULT 7
US-09-771-192-17
; Sequence 17, Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771.192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-771-192-17

Query Match 90.2%; Score 37; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYXHPF 7
Db 1 RYXHPF 7

RESULT 8
US-09-837-697A-13
; Sequence 13, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; FILE REFERENCE: 97.017-F1A
; CURRENT APPLICATION NUMBER: US/09/837.697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: All analogue
NAME/KEY: MISC FEATURE
LOCATION: (4)
; OTHER INFORMATION: Nle
US-09-837-697A-13

Query Match 90.2%; Score 37; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYXHPF 7
Db 1 RYXHPF 7

RESULT 9
US-09-837-697A-17
; Sequence 17, Application US/09837697A
; Patent No. US20020146823A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; FILE REFERENCE: 97.017-F1A
; CURRENT APPLICATION NUMBER: US/09/837.697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
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NAME/KEY: MISC FEATURE
LOCATION: (4)
; OTHER INFORMATION: Nle
US-09-837-697A-17

Query Match 90.2%; Score 37; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYXHPF 7
Db 1 RYXHPF 7

RESULT 10
US-09-900-936-13
; Sequence 13, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900.936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
NAME/KEY: MOD RES
LOCATION: (4)
; OTHER INFORMATION: Nle
US-09-900-936-13

Query Match 90.2%; Score 37; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYXHPF 7
Db 1 RYXHPF 7

RESULT 11
US-09-900-936-17
; Sequence 17, Application US/09900936
; Patent No. US20020165141A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900.936
; CURRENT FILING DATE: 2001-07-09
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; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-930-936-17

Query Match 90.2%; Score 37; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
| | | | |
DB 1 RYVGHPF 7

RESULT 12
US-09-772-819-13
; Sequence 13, Application US/09772819
; Publication No. US20030199434A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; FILE REFERENCE: 98365b
; CURRENT APPLICATION NUMBER: US/09/772.819
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: Nle
US-09-772-819-13

Query Match 90.2%; Score 37; DB 12; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
| | | | |
DB 1 RYVXHPF 7

RESULT 13
US-09-772-819-17
; Sequence 17, Application US/09772819
; Publication No. US20030199434A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; FILE REFERENCE: 98365b
; CURRENT APPLICATION NUMBER: US/09/772.819
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-772-819-17

Query Match 90.2%; Score 37; DB 12; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
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DB 1 RYVGHPF 7

RESULT 14
US-10-341-001-13
; Sequence 13, Application US/10341001
; Publication No. US20030130196A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K5
; CURRENT APPLICATION NUMBER: US/10/341.001
; CURRENT FILING DATE: 2003-01-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: Nle
US-10-341-001-13

Query Match 90.2%; Score 37; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
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DB 1 RYVXHPF 7

RESULT 15
US-10-341-001-17
; Sequence 17, Application US/10341001
; Publication No. US20030130196A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K5
; CURRENT APPLICATION NUMBER: US/10/341.001
; CURRENT FILING DATE: 2003-01-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-10-341-001-17

Query Match 90.2%; Score 37; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
| | | | |

Db 1 RYCHP 7

Search completed: November 5, 2003, 18:21:06
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:11:10 ; Search time 25 Seconds
(without alignments)
26.927 Million cell updates/sec

Title: US-09-772-819-18
Perfect score: 41
Sequence: 1 RYVAHPF 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	90.2	10	2 A60624	angiotensin - Ja
2	37	90.2	10	2 A90917	angiotensin precu
3	37	90.2	10	2 A90345	angiotensin precu
4	36	87.8	10	2 S65432	angiotensin I - ho
5	36	87.8	11	2 S07207	Crinia-angiotensin
6	36	87.8	14	2 A01250	angiotensin precu
7	36	87.8	15	2 A60834	angiotensin I prec
8	36	87.8	476	1 JC2318	angiotensin precu
9	36	87.8	477	1 ANP7	angiotensin precu
10	36	87.8	477	1 A29378	angiotensin precu
11	36	87.8	485	1 ANEU	angiotensin precu
12	35	85.4	146	2 AEG982	angiotensin precu
13	35	85.4	329	2 S28305	probable acetyltra
14	35	85.4	723	2 B88551	hypothetical prote
15	34	82.9	374	2 B82572	protein T23G5.2 li
16	33	80.5	424	2 B62190	P-protein XF2325 i
17	33	80.5	444	2 B64119	glycine hydroxymet
18	33	80.5	751	2 T02858	glucose-1-phosphat
19	32	78.0	83	1 A42645	hypothetical prote
20	32	78.0	83	2 F81664	ribosomal protein
21	32	78.0	176	1 F64725	probable NAD(P)H2
22	32	78.0	176	2 A85486	probable NAD(P)H o
23	32	78.0	176	2 A90635	probable NAD(P)H o
24	32	78.0	176	2 A10512	probable NAD(P)H o
25	32	78.0	211	2 B70563	probable fic prote
26	32	78.0	232	2 JC4755	ribosomal protein
27	32	78.0	324	2 E84918	hypothetical prote
28	32	78.0	346	2 S73760	MG285 homolog F.1-
29	32	78.0	388	1 S52149	pore protein amel

30 32 78.0 424 2 C70651
31 32 78.0 428 2 F69050
32 32 78.0 431 1 Y0EC
33 32 78.0 431 2 C91163
34 32 78.0 431 2 D86009
35 32 78.0 431 2 AH0995
36 32 78.0 482 2 S23532
37 32 78.0 516 2 AH2760
38 32 78.0 516 2 F97541
39 32 78.0 601 2 T21814
40 32 78.0 713 2 T21201
41 32 78.0 845 2 H71317
42 32 78.0 1436 2 A99115
43 31 75.6 128 2 G81220
44 31 75.6 132 2 F82800
45 31 75.6 205 2 G75535

ALIGNMENTS

RESULT 1
A60624
angiotensin I - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C:Accession: A60624
R:Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of th
A:Reference number: A60624; MUID:90284684; PMID:2191893
A:Accession: A60624
A:Molecule type: protein
A:Residues: 1-10 <TAK>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 90.2%; Score 37; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAHPF 7
Db 2 RYVHPF 8

RESULT 2
A90917
angiotensin precursor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90917; A01250
R:Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and i
A:Reference number: A90917; MUID:74127845; PMID:4361802
A:Accession: A90917
A:Molecule type: protein
A:Residues: 1-10 <NAK>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 90.2%; Score 37; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAHPF 7
Db 2 RYVHPF 8

RESULT 3

```
A90345
angiotensin precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90345; AC1250
R:Elliot, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A:Title: The amino acid sequence in a hypertensin.
A:Reference number: A90345
A:Accession: A90345
A:Molecule type: protein
A:Residues: 1-10 <ELL>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 90.2%; Score 37; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
DB 2 RYVHPF 8

RESULT 4
S65432
angiotensin I - horn fly (fragment)
C:Species: Haematobia irritans (horn fly)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65432
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.
Eur. J. Biochem. 237, 414-423, 1996
A:Title: Cloning and characterization of angiotensin-converting enzyme from the dipteran
A:Reference number: S65431; MUID:96215437; PMID:8647080
A:Accession: S65432
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <WIJ>
A:Note: the source is designated as Haematobia irritans exigua

Query Match 87.8%; Score 36; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
DB 2 RYVHPF 8

RESULT 5
S07207
Crinia-angiotensin, skin - frog (Crinia georgiana)
C:Species: Crinia georgiana
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C:Accession: S07207
R:Erspamer, V.; Meichlori, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979
A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-11
A:Reference number: S07207; MUID:80024575; PMID:488254
A:Accession: S07207
A:Molecule type: protein
A:Residues: 1-11 <ERS>
C:Superfamily: unassigned animal peptides

Query Match 87.8%; Score 36; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 0.27;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
DB 5 RYVHPF 11

A90345
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C:Accession: A92775; A01250
R:Skeggs Jr., L.F.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKE>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 87.8%; Score 36; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 0.34;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
DB 2 RYVHPF 8

RESULT 7
A60834
angiotensin I precursor - dog (fragment)
N:Alternate names: angiotensinogen I
N:Contains: angiotensin I
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C:Accession: A60834
R:Oliver, J.A.
Hypertension 11, 21-27, 1988
A:Title: Purification and partial characterization of canine angiotensinogen.
A:Reference number: A60834; MUID:88113996; PMID:3338837
A:Accession: A60834
A:Molecule type: protein
A:Residues: 1-15 <OLI>
C:Superfamily: antithrombin III
C:Keywords: glycoprotein; plasma
F:1-10/Product: angiotensin I #status predicted <MAT>

Query Match 87.8%; Score 36; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 0.37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
DB 2 RYVHPF 8

RESULT 8
JC2318
angiotensin precursor - sheep
N:Alternate names: angiotensinogen
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC2318; A25406
R:Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura,
Biochem. Biotechnol. Biochem. 58, 1884-1885, 1994
A:Title: Sequencing and expression of sheep angiotensinogen cDNA.
A:Reference number: JC2318; MUID:95072318; PMID:7765514
A:Accession: JC2318
A:Molecule type: mRNA
A:Residues: 1-476 <NAG>
A:Cross-references: DDBJ:D17520; NID:9575593; PIDN:BA04470.1; PID:g1197183
A:Experimental source: liver
A:Note: the authors translated the codon TTC for residue 465 as Leu
R:Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
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Eur. J. Biochem. 154, 597-601, 1986
A:Title: Purification and characterization of ovine angiotensinogen.
A:Reference number: A25406; MUID:86136099; PMID:3081342
A:Accession: A25406
A:Molecule type: protein
A:Residues: 25-37; 'X', 39 <PER>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:24-476/Product: angiotensinogen #status predicted <MPT>
F:25-34/Product: angiotensin #status predicted <NP2>
F:295.362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      87.8%; Score 36; DB 1; Length 476;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 26 RYVHPF 32

RESULT 9
ANRT
angiotensin precursor - rat
N:Contains: angiotensin I; angiotensin II; angiotensin III
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1983 #sequence revision 13-Jun-1983 #text_change 18-Jun-1999
R:Accession: A93945; A90456; A01251
R:Okubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A:Title: Cloning and sequence analysis of cDNA for rat angiotensinogen.
A:Reference number: A93945; MUID:83169849; PMID:6572971
A:Accession: A93945
A:Molecule type: mRNA
A:Residues: 1-477 <OHK>
A:Cross-references: GB:I000094; GB:J03704; NID:G202912; PIDN:AAA98779.1; PID:G202914
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A:Title: Rat angiotensinogen and Des(angiotensin)angiotensinogen: purification, character-
A:Reference number: A90456; MUID:82091819; PMID:6797467
A:Accession: A90456
A:Molecule type: protein
A:Residues: 25-41 <BOU>
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted in
e. I. (angiotensin-converting enzyme). Primarily in the lungs.
C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and ang
sp-1 angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma. The
ung.
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MPT>
F:25-34/Product: angiotensin I #status experimental <PP1>
F:25-32/Product: angiotensin II #status experimental <PP2>
F:26-32/Product: angiotensin III #status experimental <PP3>
F:295.319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      87.8%; Score 36; DB 1; Length 477;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 26 RYVHPF 32

RESULT 10
A29978
angiotensin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A29978
R:Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A:Title: Molecular cloning of the mouse angiotensinogen gene.
A:Reference number: A29978; MUID:88284703; PMID:3397061
A:Accession: A29978
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-477 <CLO>
A:Cross-references: GB:AF045887; GB:J03046; NID:G2842773; PIDN:AAC01765.1; PID:G2842771
C:Genetics:
A:Introns: 277/1; 366/2; 414/3
C:Superfamily: antithrombin III
C:Keywords: blood pressure control
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MAT>

Query Match      87.8%; Score 36; DB 1; Length 477;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
Db 26 RYVHPF 32

RESULT 11
ANHU
angiotensin precursor [validated] - human
N:Alternate names: angiotensinogen
N:Contains: angiotensin I; angiotensin II; angiotensin III
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1982 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
A:Accession: A35203; A31362; I37168; I37169; A60825; I39462; A90487; A90426; I34281; A
R:Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,
J. Biol. Chem. 265, 7576-7582, 1990
A:Title: Structure and expression of the human angiotensinogen gene. Identification of
A:Reference number: A35203; MUID:90237063; PMID:1692023
A:Accession: A35203
A:Molecule type: DNA
A:Residues: 1-485 <FOU>
A:Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327
R:Gaillard, I.; Clauser, E.; Corvol, P.
DNA 8, 87-99, 1989
A:Title: Structure of human angiotensinogen Gene.
A:Reference number: A31362; MUID:89170129; PMID:2924688
A:Accession: A31362
A:Molecule type: DNA
A:Residues: 1-267; 'M', 269-332; 'E', 334-485 <GAI>
A:Cross-references: GB:M24686; GB:M24687; GB:M24688
A:Note: the authors translated the codon GAA for residue 333 as Gln
R:Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.
J. Biol. Chem. 269, 28598-28605, 1994
A:Title: Identification of cell type-dependent enhancer core element located in the 3'-
A:Reference number: I37168; MUID:95050659; PMID:7961807
A:Accession: I37168
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-285 <NIB1>
A:Cross-references: EMBL:X15324; NID:G1197496; PIDN:CAA33385.1; PID:G1197497
A:Accession: I37169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 287-375 <NIB2>
A:Cross-references: EMBL:X15325; NID:G28695
R:Kunapuli, S.P.; Benedict, C.R.; Kumar, A.
Arch. Biochem. Biophys. 254, 642-646, 1987
A:Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression
A:Reference number: A60825; MUID:87212053; PMID:3579322
A:Accession: A60825
A:Molecule type: mRNA
A:Residues: 32-184 <KUNI>
R:Kunapuli, S.P.; Kumar, A.

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Circ. Res. 60, 786-790, 1987
A:Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of a second exon in the 5' region
A:Reference number: I39462; MUID:87244745; PMID:2885106
A:Accession: I39462
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-267, 'M', 269-338 <KUN2>
A:Cross-references: GB:M69110; NID:g178643; PIDN:AAAS2282.1; PID:g553181
R:Kageyama, R.; Ohkubo, H.; Nakanishi, S.
Biochemistry 23, 3603-3609, 1984
A:Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequence
A:Reference number: A90487; MUID:8500455; PMID:6093875
A:Accession: A90487
A:Molecule type: mRNA
A:Residues: 1-267, 'M', 269-485 <XAG>
A:Cross-references: GB:X02215; NID:g178639; PIDN:AAAS1731.1; PID:g178640
A:Note: It is uncertain whether Met-1 or Met-10 is the initiator
R:Teakabury, D.A.; Dart, R.A.; Travis, J.
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981
A:Title: The amino terminal amino acid sequence of human angiotensinogen.
A:Reference number: A90226; MUID:81255848; PMID:7259779
A:Accession: A90226
A:Molecule type: protein
A:Residues: 34-46, 'X', 48-50, 'S', 52-57, 'D' <TEW>
R:Hixson, J.E.; Powers, P.K.
Hum. Genet. 96, 110-112, 1995
A:Title: Detection and characterization of new mutations in the human angiotensinogen gene
A:Reference number: I54281; MUID:95331754; PMID:7607642
A:Accession: I54281
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 176-241, 'I', 243-267, 'M', 269-287, 'ANUSAG' <HIX>
A:Cross-references: GB:S78529; NID:g999316; PIDN:AAD14287.1; PID:g4261987
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted in the lungs.
e 1 (angiotensin-converting enzyme), primarily in the lungs.
C:Comment: The release of the amino-terminal residue (Asp34) from angiotensin I and angiotensin II is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels, by inducing thirst.
C:Comment: Angiotensin II and angiotensin III are equally potent in stimulating the synthesis of angiotensinogen in the liver and secreted into the plasma.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
C:Genetics:
A:Gene: GDB:AGT
A:Cross-references: GDB:118750; OMIM:106150
A:Map position: 1q42-1q43
A:Introns: 286/1; 375/2; 423/3
C:Superfamily: antithrombin III
F:1-33/Domain: (or 10-33) signal sequence; liver; plasma; vasoconstrictor
F:34-485/Product: blood pressure control; gliycoprotein; liver; plasma; vasoconstrictor
F:34-43/Product: angiotensin; #status predicted <MPT>
F:34-41/Product: angiotensin; #status experimental <PP1>
F:35-41/Product: angiotensin III; #status experimental <PP2>
F:47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 87.8%; Score 36; DB 1; Length 485;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RYVAHPF 7
Db 35 RYVTHPF 41
RESULT 12
A:Accession: A90982
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: A90982
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar AB0502; MUID:21534947; PMID:11677608
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07985.1; PID:g1650497.1; GSPDB:GN00176
C:Genetics:
A:Gene: STY4159
C:Superfamily: Escherichia coli hypothetical 16.4K protein (rife-meta intergenic region)
Query Match 85.4%; Score 35; DB 2; Length 146;
Best Local Similarity 83.3%; Pred. No. 7.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VYAHPP 7
Db 22 IYAHPP 27
RESULT 13
S28305
hypothetical protein T23G5.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 30-Sep-1993
C:Accession: S28305
R:Berks, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28296
A:Accession: S28305
A:Molecule type: DNA
A:Residues: 1-329 <BER>
A:Cross-references: EMBL:Z19158
C:Genetics:
A:Introns: 21/3; 115/3; 193/1; 235/1; 259/1
Query Match 85.4%; Score 35; DB 2; Length 329;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RYVAHPF 7
Db 10 RYXGPF 16
RESULT 14
B88551
protein T23G5.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B88551
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an erratum appeared in Science 283, 35, 1999
A:Accession: B88551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-743 <STO>
A:Cross-references: GB:chr_III; PIDN:CAA79573.1; PID:g3880120; GSPDB:GN00021; CESP:T23G5.2
C:Genetics:
A:Gene: T23G5.2
A:Map position: 3
Query Match 85.4%; Score 35; DB 2; Length 743;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAHPF 7
|:|:|
Db 10 RIYKHPF 16

RESULT 15

B82572

P-protein XF2325 [imported] - Xylella fastidiosa (strain: 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Feb-2003

C:Accession: B82572

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82572

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-374 <SIM>

A:Cross-references: GB:A8004043; GB:A8003849; NID:g9107486; PIDN:AAF85124.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2325

C:Superfamily: bifunctional chorismate mutase/prephenate dehydratase (P-protein); prephe

Query Match

Best Local Similarity 82.9%; Score 34; DB 2; Length 374;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYVAHP 6

|:|:|

Db 201 RIYAHF 206

Search completed: November 5, 2003, 13:15:29

Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:02:50 ; Search time 18 Seconds
(without alignments)

18.288 Million cell updates/sec

Title: US-09-772-819-18

Perfect score: 41

Sequence: 1 RYVAHPF 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	90.2	10	1	ANG1_BOTJA
2	37	90.2	10	1	ANG1_BOVIN
3	37	90.2	10	1	ANG1_CHICK
4	36	87.8	8	1	ANG1_BOTJA
5	36	87.8	11	1	ANG1_CRIGE
6	36	87.8	14	1	ANG1_HORSE
7	36	87.8	476	1	ANG1_SHEEP
8	36	87.8	477	1	ANG1_MOUSE
9	36	87.8	477	1	ANG1_RAT
10	36	87.8	485	1	ANG1_HUMAN
11	35	85.4	743	1	YN02_CAEEL
12	34	82.9	544	1	H15_DROME
13	33	80.5	424	1	GLYA_METTM
14	33	80.5	437	1	GLGC_HAEIN
15	33	80.5	439	1	GLGC_PASMU
16	32	78.0	83	1	RS17_CHLMU
17	32	78.0	83	1	RS17_CHLTR
18	32	78.0	176	1	YABF_ECOLI
19	32	78.0	221	1	RLIA_SCHPO
20	32	78.0	221	1	RLIB_SCHPO
21	32	78.0	346	1	Y285_MYCPN
22	32	78.0	388	1	AMSL_EWAM
23	32	78.0	423	1	GLYA_METTH
24	32	78.0	430	1	GLGC_ECOLI
25	32	78.0	431	1	GLGC_SALTI
26	32	78.0	431	1	GLGC_SALTI
27	32	78.0	516	1	SYM_AGRF5
28	32	78.0	1087	1	DP2L_THEAC
29	32	78.0	1088	1	DP2L_THEVO
30	32	78.0	1145	1	DP2L_METAC
31	32	78.0	1152	1	DP2L_METMA
32	31	75.6	255	1	YM37_MYCTU
33	31	75.6	304	1	Y191_METTH

ALIGNMENTS

RESULT 1

ANG1_BOTJA
ID _ANG1_BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
plasma of the snake Bothrops jararaca".
EL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7

Db 2 RYVHPF 8

RESULT 2

ANG1_BOVIN
ID _ANG1_BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp(1)-angiotensin II)] (Fragment).
GN AGT OR SERPIN8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;

34 31 75.6 331 1 SPFA_BACHD Q8x809 bacillus ha
35 31 75.6 360 1 STDH_YEAST P25379 saccharomyc
36 31 75.6 476 1 GLGC_YERPE Q8za77 yersinia pe
37 31 75.6 505 1 GUAA_PYRAE Q8zt92 pyrobaculum
38 31 75.6 511 1 GUAA_CAMJE Q9pn49 campylobact
39 31 75.6 521 1 GUAA_NEIMA Q9jw6C neisseria m
40 31 75.6 521 1 GUAA_NEIMB Q9jxr2 neisseria m
41 31 75.6 521 1 GUAA_XANAC Q8pk86 xanthomonas
42 31 75.6 521 1 GUAA_XANCP Q8pk86 xanthomonas
43 31 75.6 522 1 GUAA_XYLFA Q9pat6 xylella fas
44 31 75.6 525 1 GUAA_PSEAE Q9hxm6 pseudomonas
45 31 75.6 542 1 GUAA_SYNY3 P49057 synechocyst

RT "The amino acid sequence in a hypertensin.";
 RL Biochem. J. 65:246-254(1957).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A90345; A90345.
 DR PDB: 3ER5; 15-JUL-92.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON TER 10 10
 FT SEQUENCE 10 AA; 1282 MW; CEEFDD761F2DB42 CRC64;
 SQ
 Query Match 90.2%; Score 37; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 0.11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 DB 2 RYVHPF 8
 RESULT 3
 ID -ANGT CHICK STANDARD; PRT; 10 AA.
 AC P01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen (Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II))
 DE (Fragment)
 GN AGT OR SERPIN8
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]_TaxID=9031, 93934;
 RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.C.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takei Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.

CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC PIR: A60624; A60624.
 CC PIR: A90917; A90917.
 CC InterPro: IPR000215; Serpin.
 CC PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON TER 10 10
 FT SEQUENCE 10 AA; 1232 MW; CEEFDD761F2DB42 CRC64;
 SQ
 Query Match 90.2%; Score 37; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 0.11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 DB 2 RYVHPF 8
 RESULT 4
 ID -ANG2_BOTJA STANDARD; PRT; 8 AA.
 AC Q10582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide II (Fragment).
 DE Bothrops jararaca (Jararaca).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON TER 8
 FT SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;
 SQ
 Query Match 87.8%; Score 36; DB 1; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.3e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 DB 2 RYVHPF 8
 RESULT 5
 ID -ANGT CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erpamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endopeptide from the skin of the Australian
 RT frog Crinia georgiana.";
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR: S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 87.8%; Score 36; DB 1; Length 11;
 Best Local Similarity 71.4%; Pred. No. 0.18; Length 11;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 5 RYVHPF 11

RESULT 6

ANGT_HORSE
 ID ANGT_HORSE STANDARD; PRT; 14 AA.
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen (Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)) (Fragment).
 DE AGT OR SERPINAS.
 GN Equus caballus (Horse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.

RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate.";
 RL J. Exp. Med. 106:439-453(1957).
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC Plasma.

CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR: A92775; A01250.
 DR PDB: 1ER8; 15-OCT-91.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1759 MW; 2B9921F8EEFBD07 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 0.23;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 2 RYVHPF 8

RESULT 7

ANGT_SHEEP
 ID ANGT_SHEEP STANDARD; PRT; 476 AA.
 AC P20757;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen precursor (Contains: Angiotensin I (Ang I);
 DE Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-
 DE angiotensin II)).
 GN AGT OR SERPINAS.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95072318; PubMed=7765514;
 RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
 RA Murakami K., Nakamura Y.;
 RT "Sequencing and expression of sheep angiotensinogen cDNA.";
 RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
 RN [2]
 RP SEQUENCE OF 25-39.
 RX MEDLINE=86136099; PubMed=3081342;
 RA Fernley R.T., John M., Niall H.D., Coghlan J.P.;
 RT "Purification and characterization of ovine angiotensinogen.";
 RL Eur. J. Biochem. 154:597-601(1986).

CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the

CC Plasma.

CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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CC -----

DR EXBL: D17520; BAA04470.1; -

DR PIR: JC2318; JC2318.

DR InterPro: IPR000227; Angiotensngn.

DR InterPro: IPR000215; Serpin.

DR Pfam: PF00079; serpin; 1.

DR PRINTS: PR00654; ANGIOTENSNGN.

DR SMART: SM00093; SERPIN; 1.

DR PROSITE: PS00284; SERPIN; 1.

KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.

FT SIGNAL 1 24

FT CHAIN 25 476 ANGIOTENSINOGEN.

FT PEPTIDE 25 34 ANGIOTENSIN I.

FT PEPTIDE 25 32 ANGIOTENSIN II.

FT PEPTIDE 26 32 ANGIOTENSIN III.

FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 476;

Best Local Similarity 85.7%; Pred. No. 7.3;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7

DB 26 RYVHPF 32

```
RESULT 8
ANGT_MOUSE  STANDARD;  PRT;  477 AA.
ID  ANGT_MOUSE
AC  P11859;
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-OCT-1989 (Rel. 12, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Angiotensinogen precursor [Contains: Angiotensin I (Ang I);
DE  Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-
DE  angiotensin II)].
GN  AGT OR SERPINAB.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [-]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=88284703; PubMed=3397061;
RA  Cloutier W.M., Evans B.A., Haralambidis J., Richards R.I.;
RT  "Molecular cloning of the mouse angiotensinogen gene.";
RL  Genomics 2:240-248(1988).
CC  -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC  CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC  CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC  PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC  PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC  BALANCE OF BODY FLUIDS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
CC  plasma.
CC  -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  -----
EMBL; AF045887; AAC01765.1;
DR  EMBL; AF045886; AAC01765.1; JOINED.
DR  EMBL; AF045885; AAC01765.1; JOINED.
DR  EMBL; AF045884; AAC01765.1; JOINED.
DR  PIR; A29978; A29978.
DR  MGD; MGI:87963; Agt.
DR  InterPro; IPR000227; Angiotensngn.
DR  Pfam; PF00079; serpin; 1.
DR  PRINTS; PR00654; ANGIOTENSNGN.
DR  SMART; SM00093; SERPIN; 1.
DR  PROSITE; PS00284; SERPIN; FALSE NEG.
KW  Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT  SIGNAL 1 24
FT  CHAIN 25 477 ANGIOTENSINGEN.
FT  PEPTIDE 25 34 ANGIOTENSIN I.
FT  PEPTIDE 25 32 ANGIOTENSIN II.
FT  PEPTIDE 26 32 ANGIOTENSIN III.
FT  CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
FT  CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
FT  CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ  SEQUENCE 477 AA; 51980 MW; A877F4029F338607 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 477;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAH2F 7
DB 26 RYIHPF 32

RESULT 9
ANGT_RAT  STANDARD;  PRT;  477 AA.
ID  ANGT_RAT
AC  P01015;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Angiotensinogen precursor [Contains: Angiotensin I (Ang I);
DE  Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-
DE  angiotensin II)].
GN  AGT OR SERPINAB.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [-]
RP  SEQUENCE FROM N.A.
RX  STRAIN=Wistar;
RX  MEDLINE=83169849; PubMed=6572971;
RA  Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
RA  Nakanishi S.;
RT  "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
CC  SEQUENCE OF 25-34.
CC  MEDLINE=73060322; PubMed=4344907;
CC  Nakayama T., Nakajima T., Sokabe H.;
CC  "Comparative studies on angiotensins. II. Structure of rat
CC  angiotensin and its identification by DNS-method.";
CC  Chem. Pharm. Bull. 20:1579-1581(1972).
CC  -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC  CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC  CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC  PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC  PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC  BALANCE OF BODY FLUIDS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
CC  plasma.
CC  -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
EMBL; L00094; AAA98779.1;
DR  EMBL; L00091; AAA98779.1; JOINED.
DR  EMBL; L00092; AAA98779.1; JOINED.
DR  EMBL; L00093; AAA98779.1; JOINED.
DR  PIR; A93945; ANRT.
DR  InterPro; IPR000227; Angiotensngn.
DR  InterPro; IPR000215; Serpin.
DR  Pfam; PF00079; serpin; 1.
DR  PRINTS; PR00654; ANGIOTENSNGN.
DR  SMART; SM00093; SERPIN; 1.
DR  PROSITE; PS00284; SERPIN; FALSE NEG.
KW  Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
FT  SIGNAL 1 24
FT  CHAIN 25 477 ANGIOTENSINGEN.
FT  PEPTIDE 25 34 ANGIOTENSIN I.
FT  PEPTIDE 25 32 ANGIOTENSIN II.
FT  PEPTIDE 26 32 ANGIOTENSIN III.
FT  CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT  CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ  SEQUENCE 477 AA; 51981 MW; 689051A5788D693D CRC64;

Query Match 87.8%; Score 36; DB 1; Length 477;
Best Local Similarity 85.7%; Pred. No. 7.3;
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Matches      6;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

OY      1  RYIAHPF 7
DB      26  RYIHPF 32

RESULT 10
ANGT HUMAN
ID      ANGT HUMAN      STANDARD;      PRT;      485 AA.
AC      P01019; O16358; O16359; O96F91;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Angiotensinogen precursor [Contains: Angiotensin I (Ang I);
DE      Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp(1)-
DE      angiotensin II)].
GN      AGT OR SERPIN A8.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89170129; PubMed=2924688;
RA      Gaillard I., Clausen E., Corvol P.;
RT      "Structure of human angiotensinogen gene.";
RL      DNA 8:87-99(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85000455; PubMed=6089875;
RA      Kageyama R., Ohkubo H., Nakanishi S.;
RT      "Primary structure of human preangiotensinogen deduced from the
RT      cloned cDNA sequence.";
RL      Biochemistry 23:3603-3609(1984).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90237063; PubMed=1692023;
RA      Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
RA      Murakami K.;
RT      "Structure and expression of the human angiotensinogen gene.
RT      Identification of a unique and highly active promoter.";
RL      J. Biol. Chem. 265:7576-7582(1990).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E., Lu X., Gibbs R.A.,
RA      Fanej J., Helcer E., Kettner M., Madao A., Rodriguez S., Sanchez A.,
RA      Whiting R.W., Touchman J.W., Green E.D., Dickinson G.G.,
RA      Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA      Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [5]
RP      SEQUENCE OF 1-338 FROM N.A.
RX      MEDLINE=87244745; PubMed=2885106;
RA      Kunapuli S.P., Kumar A.;
RT      "Molecular cloning of human angiotensinogen cDNA and evidence for the
RT      presence of its mRNA in rat heart.";

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RL      Circ. Res. 60:786-790(1987).
RN      [6]
RP      SEQUENCE OF 34-45, AND SUBUNITS.
RX      TISSUE=Serum;
RX      MEDLINE=95293954; PubMed=7539791;
RA      Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
RA      Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT      "Identification of angiotensinogen and complement C3dg as novel
RT      proteins binding the proform of eosinophil major basic protein in
RT      human pregnancy serum and plasma.";
RL      J. Biol. Chem. 270:13645-13651(1995).
RN      [7]
RP      SEQUENCE OF 34-43.
RX      MEDLINE=69014170; PubMed=4300938;
RA      Arakawa K., Minohara A., Yamada J., Nakamura M.;
RT      "Enzymatic degradation and electrophoresis of human angiotensin I.";
RL      Biochim. Biophys. Acta 168:106-112(1968).
RN      [8]
RP      CARBOHYDRATE-LINKAGE SITES.
RX      MEDLINE=86056581; PubMed=3934016;
RA      Campbell D.J., Bounhnik J., Coezy E., Menard J., Corvol P.;
RT      "Processing of rat and human angiotensinogen precursors by microsomal
RT      membranes.";
RL      Mol. Cell. Endocrinol. 43:31-40(1985).
RN      [9]
RP      FUNCTION OF ANGIOTENSIN III.
RX      MEDLINE=75166949; PubMed=1132082;
RA      Goodfriend T.L., Peach M.J.;
RT      "Angiotensin III: (DES-Aspartic Acid-1)-Angiotensin II. Evidence and
RT      speculation for its role as an important agonist in the renin -
RT      angiotensin system.";
RL      Circ. Res. 36:38-48(1975).
RN      [10]
RP      STRUCTURE BY NMR OF ANGIOTENSIN II.
RX      MEDLINE=98151281; PubMed=9492317;
RA      Carpenter K.A., Wilkes B.C., Schiller P.W.;
RT      "The octapeptide angiotensin II adopts a well-defined structure in a
RT      phospholipid environment.";
RL      Eur. J. Biochem. 251:448-453(1998).
RN      [11]
RP      VARIANTS MET-207; THR-268 AND CYS-281.
RX      MEDLINE=93008239; PubMed=1394429;
RA      Jeunemaitre X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,
RA      Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
RA      Lalouel J.-M., Corvol P.;
RT      "Molecular basis of human hypertension: role of angiotensinogen.";
RL      Cell 71:169-180(1992).
RN      [12]
RP      VARIANT THR-268.
RX      MEDLINE=93291876; PubMed=8513325;
RA      Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
RA      Farrington P.F., Ogasawara M., Suzuki K., Tomoda S., Berrebi S.,
RA      Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
RT      "A molecular variant of angiotensinogen associated with
RT      preeclampsia.";
RL      Nat. Genet. 4:59-61(1993).
RN      [13]
RP      VARIANTS ILE-242; ARG-244 AND CYS-281.
RX      MEDLINE=95331754; PubMed=7607642;
RA      Hixson J.E., Powers P.K.;
RT      "Detection and characterization of new mutations in the human
RT      angiotensinogen gene (AGT)";
RL      Hum. Genet. 96:110-112(1995).
RN      [14]
RP      CHARACTERIZATION OF VARIANT CYS-281.
RX      MEDLINE=96199253; PubMed=8621667;
RA      Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T.,
RA      Celerier J., Pau B., Corvol P., Clauser E., Jeunemaitre X.;
RT      "The natural mutation Y248C of human angiotensinogen leads to abnormal
RT      glycosylation and altered immunological recognition of the protein.";
RL      J. Biol. Chem. 271:9838-9844(1996).
CC      -/- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC      CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN

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CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -!- FUNCTION: Angiotensin III stimulates aldosterone release.
 CC -!- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2
 CC heterotrimer with the proform of PRG2 and as a complex (probably
 CC a 2:2:2 heterohexamer) with pro-PRG2 and C3dg.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
 CC ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
 CC (PIH) (PREECLAMPSIA).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
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 CC EMBL; K02215; AAA51679.1; -
 CC EMBL; M24689; AAA51679.1; -
 CC EMBL; M24686; AAA51679.1; JOINED.
 CC EMBL; M24687; AAA51679.1; JOINED.
 CC EMBL; M24688; AAA51679.1; JOINED.
 CC EMBL; X15324; CAA33385.1; -
 CC EMBL; X15325; CAA33385.1; JOINED.
 CC EMBL; X15326; CAA33385.1; JOINED.
 CC EMBL; X15327; CAA33385.1; JOINED.
 CC EMBL; M69110; AAA52282.1; -
 CC EMBL; BC011519; AAH1519.1; -
 CC EMBL; S78529; AAD14287.1; -
 CC EMBL; S78530; AAD14288.1; -
 CC PIR; A35203; ANHU.
 CC SWISS-2DPAGE; P01019; HUMAN.
 CC Genew; HGNC:333; AGT.
 CC MIM; 106150; -
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0004867; F:serine protease inhibitor activity; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 CC GO; GO:0007287; P:cell-cell signaling; TAS.
 CC GO; GO:0007565; P:pregnancy; TAS.
 CC GO; GO:0008217; P:regulation of blood pressure; TAS.
 CC InterPro; IPR000227; Angiotensngn.
 CC InterPro; IPR000215; Serpin.
 CC Pfam; PF00079; serpin; 1
 CC PRINTS; PR00654; ANGIOTENSNGN.
 CC SMART; SM00093; SERPIN; 1.
 CC PROSITE; PS00284; SERPIN; 1.
 CC Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;
 CC Disease mutation; Polymorphism.
 CC SIGNAL 1 33
 CC FT CHAIN 34 485 ANGIOTENSINOGEN.
 CC FT PEPTIDE 34 43 ANGIOTENSIN I.
 CC FT PEPTIDE 34 41 ANG-OTENSIN II.
 CC FT PEPTIDE 35 41 ANGIOTENSIN III.
 CC FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .).
 CC FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .).

Query Match 87.8%; Score 36; DB 1; Length 485;
 Best Local Similarity 85.7%; Pred. No. 7.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 35 RYVTHPF 41

RESULT 11
 YN02 CAEL STANDARD; PRT; 743 AA.
 AC Q03606; Q03608; -
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypothetical 84.0 kDa protein T23G5.2 in chromosome III.
 GN T23G5.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Feloderinae; Caenorhabditis.
 OC NCBI_taxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Fraser A.,
 Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 Fulton L., Gardner A., Green P., Hawkins T., Hallier L., Jier M.,
 Johnston L., Jones M., Kersey J., Kirsten J., Laisner N.,
 Latheille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 Parsons J., Percy C., Rifkin L., Roodra A., Saunders D., Showkeen R.,
 Sims M., Snelson N., Smith A., Smith M., Sonhammer E., Staden K.,
 Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 Waterston R., Watson A., Weinstock L., Wilkins-Sproat J.,
 Wchidman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38 (1994).
 CC -!- SIMILARITY: Contains 1 CRAL-TRIO domain.
 CC -!- SIMILARITY: Contains 1 GOLD domain.
 CC -!- SIMILARITY: Contains 1 PRELI/MSF1 domain.
 CC -----
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 CC -----
 CC EMBL; Z19158; CAA79573.1; -
 CC PIR; B88551; B88551.
 CC WormPep; T23G5.2; CEG1099.
 CC InterPro; IPR001251; CRAL-TRIO.
 CC InterPro; IPR006797; MSF1.
 CC InterPro; IPR001071; RetBind/toctrans.
 CC Pfam; PF00650; CRAL-TRIO; 1.
 CC Pfam; PF03765; CRAL-TRIO_N; 1.
 CC Pfam; PF04707; MSF1; 1.
 CC PRINTS; PR00180; CRETINALDHP.
 CC SMART; SM00516; SEC14; 1.
 CC PROSITE; PS50191; CRAL-TRIO; 1.
 CC PROSITE; PS50866; GOLD; 1.
 CC PROSITE; PS50904; PRELI_MSFI; 1.
 CC Hypothetical protein.
 CC KW DOMAIN 1 175 PRELI/MSFI.
 CC FT DOMAIN 343 519 CRAL-TRIO.
 CC FT DOMAIN 548 705 GOLD.
 CC SEQUENCE 743 AA; 83984 MW; 4121F9F94DE2B587 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 743;
 Best Local Similarity 71.4%; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 10 RYKHPF 16

RESULT 12

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H15 DROME
ID H15 DROME STANDARD; PRT; 544 AA.
AC Q94890;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE T-box protein H15.
GN H15.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Brook W.J., Cohen S.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 T-box domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: X98766; CAA67304.1; -
CC HSSP: P24781; 1XBR.
CC TRANSFAC: T04412; -
CC FLYBASE: FBgn0016660; H15.
CC InterPro: IPR001699; TF_T-box.
CC Pfam: PF00907; T-box; 1.
CC PRINTS: PR00937; TBOX.
CC SMART: SM00425; TBOX; 1.
CC PROSITE: PS01283; TBOX 1; 1.
CC PROSITE: PS01264; TBOX_2; FALSE_NEG.
CC PROSITE: PS0252; TBOX_3; 1.
CC DNA-binding; Nuclear protein.
CC DOMAIN 56 59 POLY-ALA.
CC FT DOMAIN 83 91 POLY-GLN.
CC FT DOMAIN 118 125 POLY-PRO.
CC FT DNA_BIND 170 356 T-BOX.
CC FT DOMAIN 242 245 POLY-PRO.
CC FT DOMAIN 436 443 POLY-PRO.
CC SEQUENCE 544 AA; 600.0 MW; 4D4EDB8E78244132 CRC64;

Query Match 82.9%; Score 34; DB 1; Length 544;
Best Local Similarity 83.3%; P-red. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYVAFP 6
Db 247 RYVAFP 252

RESULT 13
GLYA_METTM STANDARD; PRT; 424 AA.
AC P50436;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
DE (SHMT).
DE GLYA.
GN GLYA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]

SEQUENCE FROM N.A.
RX MEDLINE=96184910; PubMed=8617278;
RA Vaupel M., Dietz H., Linder D., Thauer R.K.;
RT "Primary structure of cyclohydrolase (Mch) from Methanobacterium
RT thermoautotrophicum (strain Marburg) and functional expression of the
RT mch gene in Escherichia coli.";
RL Eur. J. Biochem. 236:294-300(1996).
CC -!- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine +
CC H(2)O = tetrahydrofolate + L-serine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS,
CC HORMONES AND OTHER COMPONENTS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SHMT FAMILY.
CC -----
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CC -----
CC EMBL: X92C83; CAA63066.1; -
CC HSSP: P00477; 1DFO.
CC HAMAP: MF_00051; 1.
CC InterPro: IPR001085; Gly_HyMettransf.
CC Pfam: PF00464; SHMT; 1.
CC PROSITE: PS00096; SHMT; 1.
CC T-transferase; Pyridoxal phosphate; One-carbon metabolism.
CC BINDING 227 227 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 424 AA; 47076 MW; BF9867A411587956 CRC64;

Query Match 80.5%; Score 33; DB 1; Length 424;
Best Local Similarity 57.1%; P-red. No. 26;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY - RYVAFP 7
Db 237 RYVAFP 143

RESULT 14
GLGC_HAEIN STANDARD; PRT; 437 AA.
AC P43756;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glucose-1-phosphate adenyltransferase (EC 2.7.7.27) (ADP-glucose
DE synthase) (ADP-glucose pyrophosphorylase) (ADPGlc Ppase).
DE GLGC OR H11359.
GN Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.P., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.I., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RN "Whole-genome random sequencing and assembly of Haemophilus influenzae
RN Rd.";
RN Science 269:496-512(1995).

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CC -!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =
CC diphosphate + ADP-glucose.
CC -!- PATHWAY: Glycogen biosynthesis; first step.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-
CC PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL; U32815; AAC23006.1; ALT_INIT.
DR PIR; B64119; B64119.
DR TIGR; H11359; -.
DR HAMAP; MF_00624; -.
DR InterPro; IPR005836; ADP_Glu_pyrop.
DR InterPro; IPR005835; NTP_transferase.
DR Pfam; PF00483; NTP_transferase; 1.
DR PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; 1.
DR PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
DR PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.
KW Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
KW Complete proteome.
SQ SEQUENCE 437 AA; 49107 MW; E5E284ACESAD1D9 CRC64;
Query Match 80.5%; Score 33; DB 1; Length 437;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VYAHPF 7
DB 254 LVAHPF 259
-----
RESULT 15
GLGC_PASMU STANDARD; PRT; 439 AA.
AC Q9CN92;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose
DE synthase) (ADP-glucose pyrophosphorylase) (ADPGlc PCase).
GN GLGC OR PM0543.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Em70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
CC -!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =
CC diphosphate + ADP-glucose.
CC -!- PATHWAY: Glycogen biosynthesis; first step.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-
CC PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL; AE006089; AAK02627.1; -.

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DR HAMAP; MF_00624; -.
DR InterPro; IPR005836; ADP_Glu_pyrop.
DR InterPro; IPR005835; NTP_transferase.
DR Pfam; PF00483; NTP_transferase; 1.
DR PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; 1.
DR PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
DR PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.
KW Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
KW Complete proteome.
SQ SEQUENCE 439 AA; 49405 MW; 95PAD1B30C1336BF CRC64;
Query Match 80.5%; Score 33; DB 1; Length 439;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VYAHPF 7
DB 257 LVAHPF 262
-----
Search completed: November 5, 2003, 18:12:51
Job time : 20 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:10:26 ; Search time 53 Seconds

(without alignments)
34.082 Million cell updates/sec

Title: US-09-772-819-18

Perfect score: 41

Sequence: 1 RYVAHPF 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	90.2	10	13	Q9PS07 alligator m
2	37	90.2	454	13	Q8JH29 brachydario
3	36	87.8	14	5	Q10757 theromyzon
4	36	87.8	222	11	Q8BX66 mus musculu
5	36	87.8	244	11	Q8CD22 mus musculu
6	36	87.8	245	6	Q95J13 pan troglod
7	36	87.8	477	4	Q96FD5 Q99J07 homo sapien
8	36	87.8	477	11	Q8VCN0 mus musculu
9	36	87.8	485	6	Q9GLN8 Q9GLN8 pan troglod
10	36	87.8	485	6	Q9GLP7 pan troglod
11	36	87.8	485	6	Q9GLP6 Q9GLP6 gorilla gor
12	36	87.8	486	6	Q9TSZ0 callithrix
13	36	87.8	716	11	Q99J07 mus musculu
14	36	87.8	719	11	Q9DBQ0 Q9DBQ0 mus musculu
15	35	85.4	146	16	Q8ZLA3 Q8ZLA3 salmonella
16	35	85.4	146	16	Q8Z2A6 Q8Z2A6 salmonella

17	34	82.9	269	5	Q8IMU0
18	34	82.9	374	16	Q9PB20
19	34	82.9	660	5	Q9VNR3
20	33	80.5	113	2	Q8KNT2
21	33	80.5	185	17	Q8UIA7
22	33	80.5	325	2	Q93H46
23	33	80.5	439	16	Q9CN92
24	33	80.5	728	5	Q9VFT7
25	33	80.5	751	5	Q60975
26	33	80.5	842	5	Q8ISV4
27	33	80.5	997	10	Q94HV1
28	33	80.5	1074	10	Q8SSS8
29	33	80.5	1144	2	Q9AN19
30	32	78.0	176	16	Q8ZRW3
31	32	78.0	176	16	Q8Z9K1
32	32	78.0	176	16	Q8XA24
33	32	78.0	177	2	Q9X755
34	32	78.0	211	16	Q06366
35	32	78.0	212	17	Q8Z2M9
36	32	78.0	299	11	Q8BX64
37	32	78.0	331	12	Q71094
38	32	78.0	336	17	Q8TTT5
39	32	78.0	358	10	Q8Z239
40	32	78.0	395	8	Q9TMS7
41	32	78.0	401	2	Q30774
42	32	78.0	424	16	P95084
43	32	78.0	431	16	Q8Z233
44	32	78.0	482	10	Q39499
45	32	78.0	508	5	Q9BLR4

ALIGNMENTS

RESULT 1

Q9PS07 PRELIMINARY; PRT; 10 AA.
AC Q9PS07;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Angiotensin I, ANG I.
CS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RX MEDLINE=93307610; PubMed=8319878;
RA Takei Y., Silldorff B.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA Stephens G.A., Sakakibara S.;
RT "New angiotensin I isolated from a reptile, Alligator
mississippiensis".
RL Gen. Comp. Endocrinol. 90:214-219(1993).
SQ SEQUENCE 10 AA; 12.6 MW; CEE38DD761F2DB42 CRC64;

Query Match 90.2%; Score 37; DB 13; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.54;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAHPF 7
Db 2 RYVHPF 8

RESULT 2

Q8JH29 PRELIMINARY; PRT; 454 AA.

ID Q8JH29
AC Q8JH29;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Angiotensinogen precursor.

OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen M., Vallon V., Schnermann J.B., Endo Y., Smart J., Smart A.,
 RA Briggs J.P.;
 RA "Catepsin D is responsible for angiotensin generation in zebrafish."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERP-N FAMILY.
 DR EMBL; AY049731; AAL12168.1; -.
 DR InterPro; IPR000227; Angiotensin.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR PRINTS; PRO0654; ANGIOTENSNGN.
 DR SMART; SM03093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 28 ANGIOTENSIN I.
 SQ SEQUENCE 454 AA; 51058 MW; 6E8A1D4E3E2E14E38 CRC64;
 Query Match 90.2%; Score 37; DB 13; Length 454;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 DB 20 RYVHPF 26
 RESULT 3
 Q10757 PRELIMINARY; PRT; 14 AA.
 AC Q10757;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Angiotensinogen (Fragment).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95365039; PubMed=7637887;
 RA Laurent V., Bulet P., Salzet M.A.;
 RA "A comparison of the leech Theromyzon tessulatum angiotensin I-like
 RT molecule with forms of vertebrate angiotensinogens: a hormonal system
 RT conserved in the course of evolution."
 RL Neurosci. Lett. 190:175-178 (1995).
 RN [2]
 RP SEQUENCE OF 1-10.
 RC TISSUE=Brain;
 RX MEDLINE=96201949; PubMed=8612806;
 RA Laurent V., Salzet M.;
 RA "Metabolism of angiotensins by head membranes of the leech Theromyzon
 RT tessulatum."
 RL FEBS Lett. 384:123-127 (1996).
 CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
 KW Glycoprotein; Serpin.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1763 MW; 335109DEBEEFBD7 CRC64;
 Query Match 87.8%; Score 36; DB 5; Length 14;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 DB 2 RYVHPF 8

RESULT 4
 Q8BXE6 PRELIMINARY; PRT; 222 AA.
 ID Q8BXE6;
 AC Q8BXE6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE SEC14-like protein 1 homolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK047396; BAC33044.1; -.
 SQ SEQUENCE 222 AA; 25370 MW; BFCF5E2530BEC4A CRC64;
 Query Match 87.8%; Score 36; DB 11; Length 222;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RYVAHPF 7
 DB 10 RYVHPF 16
 RESULT 5
 Q8CDZ2 PRELIMINARY; PRT; 244 AA.
 ID Q8CDZ2;
 AC Q8CDZ2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK029331; BAC26399.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 244 AA; 28067 MW; BFBF32560A392D6C CRC64;
 Query Match 87.8%; Score 36; DB 11; Length 244;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VVAHPF 7
 DB 173 VVAHPF 178
 RESULT 6
 Q95J13 PRELIMINARY; PRT; 245 AA.
 ID Q95J13
 AC Q95J13;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Angiotensinogen (Fragment).
 GN REN.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=504, and 505;
 RA Satta Y.;
 RT "Comparator of DNA and protein polymorphisms between humans and
 RL chimpanzees.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AB062027; BAB55856.1; -.
 DR EMBL; AB062028; BAB55857.1; -.
 DR InterPro; IPR000227; Angiotensn.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR PRINTS; PR00654; ANGIOTENSNGN.
 DR Protease inhibitor; Serine protease inhibitor; Serpin.
 KW NON_TER 245 245
 FT SEQUENCE 245 AA; 26317 MW; E0923909803E0B CRC64;

Query Match 87.8%; Score 36; DB 6; Length 245;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 35 RYVHPF 41

RESULT 7
 Q96FD5 PRELIMINARY; PRT; 477 AA.
 AC Q96FD5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to angiotensinogen.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; BC011231; AAH11231.1; -.
 DR InterPro; IPR000227; Angiotensn.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR PRINTS; PR00654; ANGIOTENSNGN.
 DR Protease inhibitor; Serine protease inhibitor; Serpin.
 KW Protease inhibitor; Serine protease inhibitor; Serpin.
 SQ SEQUENCE 477 AA; 51985 MW; AB798B70592FDE2 CRC64;

Query Match 87.8%; Score 36; DB 4; Length 477;
 Best Local Similarity 85.7%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 26 RYVHPF 32

RESULT 8
 Q8VCN0

ID Q8VCN0 PRELIMINARY; PRT; 477 AA.
 AC Q8VCN0;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Angiotensinogen).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; BC019496; AAH19496.1; -.
 DR EMBL; BC028877; AAH28877.1; -.
 DR InterPro; IPR000227; Angiotensn.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR PRINTS; PR00654; ANGIOTENSNGN.
 DR Hypothetical protein; Protease inhibitor; Serine protease inhibitor;
 KW Serpin.
 SQ SEQUENCE 477 AA; 51985 MW; AB798B70592FDE2 CRC64;

Query Match 87.8%; Score 36; DB 11; Length 477;
 Best Local Similarity 85.7%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYVAHPF 7
 DB 26 RYVHPF 32

RESULT 9
 Q9GLN8 PRELIMINARY; PRT; 485 AA.
 AC Q9GLN8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Angiotensinogen.
 GN AGT.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20469400; PubMed=11013071;
 RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
 RA Jeunemaitre X.;
 RT "Human-Chimpanzee DNA sequence variation in the four major genes of
 the renin angiotensin system.";
 RL Genomics 69:14-26(2000).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AF193461; AAG30306.1; -.
 DR EMBL; AF193458; AAG30306.1; JOINED.
 DR EMBL; AF193459; AAG30306.1; JOINED.
 DR EMBL; AF193460; AAG30306.1; JOINED.
 DR InterPro; IPR000227; Angiotensn.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR PRINTS; PR00654; ANGIOTENSNGN.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Protease inhibitor; Serine protease inhibitor; Serpin.

```
SQ SEQUENCE 485 AA; 53110 MW; C14C67E49A53F05F CRC64;
Query Match 87.8%; Score 36; DB 6; Length 485;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYAHPP 7
   ||| |||
Db 35 RYIHPP 41

RESULT 10
Q9GLP7 PRELIMINARY; PRT; 485 AA.
AC Q9GLP7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Angiotensinogen.
GN AGT.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [2]
RP SEQUENCE FROM N.A.
DR Shattuck-Eidens D., McGrail M., Stone S.;
RT "Germline mutations in the angiotensinogen gene cause predisposition
RT to type 1 diabetes mellitus."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF188487; AAC29056.1; -.
DR InterPro; IPR000227; Angiotensn.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PRINTS; PR00654; ANGIOTENSGN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 485 AA; 53140 MW; 49EF554AF31F8ADC CRC64;

Query Match 87.8%; Score 36; DB 6; Length 485;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYAHPP 7
   ||| |||
Db 35 RYIHPP 41

RESULT 11
Q9GLP6 PRELIMINARY; PRT; 485 AA.
AC Q9GLP6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Angiotensinogen.
GN AGT.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
DR Shattuck-Eidens D., McGrail M., Stone S.;
RT "Germline mutations in the angiotensinogen gene cause predisposition
RT to type 1 diabetes mellitus."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF188488; AAC29057.1; -.
DR InterPro; IPR000227; Angiotensn.
DR InterPro; IPR000215; Serpin.
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DR PRINTS; PR00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 485 AA; 53186 MW; 53BC9235271C8255 CRC64;

Query Match 87.8%; Score 36; DB 6; Length 485;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYAHPP 7
   ||| |||
Db 35 RYIHPP 41

RESULT 12
Q9TSZ0 PRELIMINARY; PRT; 486 AA.
AC Q9TSZ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Angiotensinogen precursor.
GN ANGR.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065005; PubMed=10598135;
RA Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;
RT "Cloning and characterization of marmoset renin: comparison with human
RT renin."
RL J. Cardiovasc. Pharmacol. 34:893-897(1999).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AJ132343; CAB64880.1; -.
DR InterPro; IPR000227; Angiotensn.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PRINTS; PR00654; ANGIOTENSGN.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 486 ANGIOTENSINOGEN.
SQ SEQUENCE 486 AA; 53374 MW; 5408129B2F71F88B CRC64;

Query Match 87.8%; Score 36; DB 6; Length 486;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RYAHPP 7
   ||| |||
Db 35 RYIHPP 41

RESULT 13
Q99J07 PRELIMINARY; PRT; 716 AA.
AC Q99J07;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RIKEN CDNA 1200017E04 gene.
GN 1200017E04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RA Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC005766; AA05766.1; -
 DR MGD; MGI:1921386; 1200017E04Rik.
 DR InterPro; IPR001251; CRAL_TRIO.
 DR InterPro; IPR006797; MSF1.
 DR InterPro; IPR001071; RetBind/tocTrans.
 DR Pfam; PF00650; CRAL_TRIO; 1.
 DR Pfam; PF03765; CRAL_TRIO_N; 1.
 DR Pfam; PF04707; MSF1; 1.
 DR PRINTS; PR00180; CRETINALDHP.
 DR SMART; SM00516; SEC14; 1.
 DR PROSITE; PS50191; CRAL_TRIO; 1.
 SQ SEQUENCE 716 AA; 81275 MW; 8CA325D06ABFE8E4 CRC64;

Query Match 87.8%; Score 36; DB 11; Length 716;
 Best Local Similarity 85.7%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAHPF 7
 Db 10 RYVKHPF 16
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RESULT 14
 ID Q9DBQ0 PRELIMINARY; PRT; 719 AA.
 AC Q9DBQ0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 1200017E04Rik Protein.
 GN 1200017E04Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukurishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojochi T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bejunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK004818; BAB23589.1; -
 DR MGD; MGI:1921386; 1200017E04Rik.
 DR InterPro; IPR001251; CRAL_TRIO.
 DR InterPro; IPR006797; MSF1.
 DR Pfam; PF00650; CRAL_TRIO; 1.
 DR Pfam; PF03765; CRAL_TRIO_N; 1.
 DR Pfam; PF04707; MSF1; 1.
 DR SMART; SM00516; SEC14; 1.
 DR PROSITE; PS50191; CRAL_TRIO; 1.
 SQ SEQUENCE 719 AA; 81750 MW; 6ACB31D4F5BAB7F8 CRC64;

Query Match 87.8%; Score 36; DB 11; Length 719;

Best Local Similarity 85.7%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAHPF 7
 Db 10 RYVKHPF 16
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RESULT 15
 ID Q8ZLA3 PRELIMINARY; PRT; 146 AA.
 AC Q8ZLA3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative acetyltransferase.
 GN YIAC OR STM3643.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AEG08869; AAL22503.1; -
 DR InterPro; IPR000182; GCN5acetyltransf.
 DR Pfam; PF00583; Acetyltransf; 1.
 KW Transferase; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 146 AA; 16945 MW; BC7F24C3C91EF375 CRC64;

Query Match 85.4%; Score 35; DB 16; Length 146;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VYAHFP 7
 Db 22 IYAHFP 27
 ||| |||

Search completed: November 5, 2003, 18:14:56
 Job time : 57 secs